

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/538,370
Source: P4710
Date Processed by STIC: 6/28/05

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PCT

RAW SEQUENCE LISTING

DATE: 06/28/2005

PATENT APPLICATION: US/10/538,370

TIME: 16:11:08

Input Set : N:\AMC\538370.txt

Output Set: N:\CRF4\06282005\J538370.raw

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3 <110> APPLICANT: Emtage, Peter C.R.
6 <120> TITLE OF INVENTION: METHODS OF IMMUNOTHERAPY AND DIAGNOSIS USING TARGETING OF
CELLS THAT
7     EXPRESS LAX
9 <130> FILE REFERENCE: HYS-67/PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/538,370
C--> 12 <141> CURRENT FILING DATE: 2005-06-13
14 <150> PRIOR APPLICATION NUMBER: 10/304,234
15 <151> PRIOR FILING DATE: 2002-11-26
17 <150> PRIOR APPLICATION NUMBER: 10/128,558
18 <151> PRIOR FILING DATE: 2002-04-22
20 <150> PRIOR APPLICATION NUMBER: 60/339,453
21 <151> PRIOR FILING DATE: 2001-12-11
23 <160> NUMBER OF SEQ ID NOS: 8
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2071
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (440)..(1636)
35 <223> OTHER INFORMATION:
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40 ctgctttggg tgttgaagga agacgagctt ctcacggagc ctctcttgag cctcttggca      120
42 gtttccccct ctgtgcccct cacgtttcca ccagaaacgt gaaggcagag gccacagatt      180
44 ctccctgagc cacctcactt ggaagcacca tgtccggatg agatcgact tcttgcagtg      240
46 ggcattagcc acgtccaggt agaaccaaac ctgttgcttt tgtatgttgg gtcaacttgg      300
48 cctgacgttt cagaggtaga cagagatag ggagttggaa gcaggatgtc cggatgagat      360
50 cgcacttctt gcagagggca ttatcgctcg agaaacttag aagctgaagc cagagagcat      420
52 ctcaaagggt cctgataca atg gat ggt gtc act cca acc ctt tcg aca atc      472
53                               Met Asp Gly Val Thr Pro Thr Leu Ser Thr Ile
54                               1               5               10
56 aga ggg agg acc ttg gag tcc agc act ctg cat gtg act ccc cgc agc      520
57 Arg Gly Arg Thr Leu Glu Ser Ser Thr Leu His Val Thr Pro Arg Ser
58                               15               20               25
60 ctg gac aga aat aaa gac cag atc acc aac atc ttt tcc ggg ttt gcg      568
61 Leu Asp Arg Asn Lys Asp Gln Ile Thr Asn Ile Phe Ser Gly Phe Ala
62                               30               35               40
64 gga ctc ctc gcc atc ctc ctg gtc gtt gcg gtt ttc tgc atc ttg tgg      616
65 Gly Leu Leu Ala Ile Leu Leu Val Val Ala Val Phe Cys Ile Leu Trp
66                               45               50               55
68 aat tgg aat aaa cgg aag aag cga caa gtt cct tac ctc cga gtt acc      664

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69	Asn	Trp	Asn	Lys	Arg	Lys	Lys	Arg	Gln	Val	Pro	Tyr	Leu	Arg	Val	Thr	
70	60					65				70					75		
72	gtc	atg	ccc	ttg	ctg	act	ttg	cca	caa	acc	aga	caa	aga	gcc	aaa	aat	712
73	Val	Met	Pro	Leu	Leu	Thr	Leu	Pro	Gln	Thr	Arg	Gln	Arg	Ala	Lys	Asn	
74				80					85					90			
76	att	tat	gac	atc	ttg	cct	tgg	cga	cag	gaa	gac	ctg	ggg	aga	cat	gag	760
77	Ile	Tyr	Asp	Ile	Leu	Pro	Trp	Arg	Gln	Glu	Asp	Leu	Gly	Arg	His	Glu	
78				95					100					105			
80	tcg	agg	agt	atg	cgc	att	ttc	agt	act	gag	agc	ctc	ctc	tcc	aga	aat	808
81	Ser	Arg	Ser	Met	Arg	Ile	Phe	Ser	Thr	Glu	Ser	Leu	Leu	Ser	Arg	Asn	
82			110					115						120			
84	tct	gag	agc	ccg	gag	cat	gtg	ccc	tcc	caa	gca	ggc	aat	gcc	ttc	cag	856
85	Ser	Glu	Ser	Pro	Glu	His	Val	Pro	Ser	Gln	Ala	Gly	Asn	Ala	Phe	Gln	
86		125					130					135					
88	gag	cat	aca	gcc	cac	atc	cat	gcc	aca	gag	tac	gcg	gtg	ggg	atc	tat	904
89	Glu	His	Thr	Ala	His	Ile	His	Ala	Thr	Glu	Tyr	Ala	Val	Gly	Ile	Tyr	
90	140					145				150					155		
92	gac	aac	gcc	atg	gtc	ccc	cag	atg	tgt	ggg	aac	ctc	act	ccc	tcg	gca	952
93	Asp	Asn	Ala	Met	Val	Pro	Gln	Met	Cys	Gly	Asn	Leu	Thr	Pro	Ser	Ala	
94				160					165					170			
96	cac	tgc	atc	aat	gtc	aga	gct	tcc	aga	gac	tgc	gca	agc	att	tct	tca	1000
97	His	Cys	Ile	Asn	Val	Arg	Ala	Ser	Arg	Asp	Cys	Ala	Ser	Ile	Ser	Ser	
98			175					180						185			
100	gag	gat	tcg	cat	gat	tat	gtc	aat	gtc	ccc	aca	gca	gaa	gag	att	gct	1048
101	Glu	Asp	Ser	His	Asp	Tyr	Val	Asn	Val	Pro	Thr	Ala	Glu	Glu	Ile	Ala	
102			190					195						200			
104	gag	act	cta	gct	tct	acc	aaa	agc	cct	tcc	aga	aat	ctc	ttt	gtt	ctt	1096
105	Glu	Thr	Leu	Ala	Ser	Thr	Lys	Ser	Pro	Ser	Arg	Asn	Leu	Phe	Val	Leu	
106		205					210					215					
108	ccc	agt	acc	cag	aag	ctg	gag	ttt	act	gag	gaa	aga	gat	gag	ggc	tgt	1144
109	Pro	Ser	Thr	Gln	Lys	Leu	Glu	Phe	Thr	Glu	Glu	Arg	Asp	Glu	Gly	Cys	
110	220					225				230				235			
112	gga	gat	gct	ggg	gac	tgc	acc	agt	ttg	tat	tct	cca	gga	gct	gag	gac	1192
113	Gly	Asp	Ala	Gly	Asp	Cys	Thr	Ser	Leu	Tyr	Ser	Pro	Gly	Ala	Glu	Asp	
114				240					245					250			
116	agt	gat	tca	ctc	agc	aat	gga	gaa	ggg	tct	tct	cag	atc	tca	aat	gac	1240
117	Ser	Asp	Ser	Leu	Ser	Asn	Gly	Glu	Gly	Ser	Ser	Gln	Ile	Ser	Asn	Asp	
118			255					260						265			
120	tat	gtc	aac	atg	aca	ggg	ttg	gat	ctc	agc	gcc	atc	cag	gaa	agg	cag	1288
121	Tyr	Val	Asn	Met	Thr	Gly	Leu	Asp	Leu	Ser	Ala	Ile	Gln	Glu	Arg	Gln	
122			270					275						280			
124	ctc	tgg	gtg	gct	ttt	cag	tgc	tgc	aga	gac	tat	gaa	aat	gtt	cca	gca	1336
125	Leu	Trp	Val	Ala	Phe	Gln	Cys	Cys	Arg	Asp	Tyr	Glu	Asn	Val	Pro	Ala	
126		285					290					295					
128	gca	gat	ccc	agt	gga	agc	cag	cag	cag	gct	gag	aaa	gat	gtg	cca	tcc	1384
129	Ala	Asp	Pro	Ser	Gly	Ser	Gln	Gln	Gln	Ala	Glu	Lys	Asp	Val	Pro	Ser	
130	300					305				310				315			
132	tca	aac	ata	ggg	cat	gtc	gag	gac	aag	aca	gat	gat	ccc	ggg	acc	cat	1432
133	Ser	Asn	Ile	Gly	His	Val	Glu	Asp	Lys	Thr	Asp	Asp	Pro	Gly	Thr	His	

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134          320          325          330
136 gtc caa tgt gtc aaa agg aca ttc ctt gct tca ggg gat tat gca gac 1480
137 Val Gln Cys Val Lys Arg Thr Phe Leu Ala Ser Gly Asp Tyr Ala Asp
138          335          340          345
140 ttt cag cca ttc aca cag agt gag gac agt cag atg aaa cat aga gaa 1528
141 Phe Gln Pro Phe Thr Gln Ser Glu Asp Ser Gln Met Lys His Arg Glu
142          350          355          360
144 gag atg tca aat gag gac tcc agt gac tat gaa aat gtg cta act gcc 1576
145 Glu Met Ser Asn Glu Asp Ser Ser Asp Tyr Glu Asn Val Leu Thr Ala
146          365          370          375
148 aag tta gga ggc agg gac tct gag cag ggg cct ggc act cag ctc ctt 1624
149 Lys Leu Gly Gly Arg Asp Ser Glu Gln Gly Pro Gly Thr Gln Leu Leu
150 380          385          390          395
152 cct gat gaa tga agaccaggt acccagccat aaagccacat tgagtagtct 1676
153 Pro Asp Glu
156 atcccatagg attgactact gcagagtcta gtgcagaccc gtgatcacct tagtgcttca 1736
158 gtggattcac tggtagatt aaaaagaggc tgagatgagc agtgaactaa gaggccacac 1796
160 aaaagcagag gtttggaat tccagaaggg aattcttctc aagcagagtg tggttatctc 1856
162 ctgtaccagc ctaagaatgt ttgctgaaac tgcttcctag aactgtgaag aaagcaggaa 1916
164 agtagtgcac agtagtctaa gattattacc ttcattaata ccaacaggct gcaaagcaag 1976
166 agtatagatt attgtataat ccagtcagag gtcaaaagga aggaagaagt tggagtggag 2036
168 tggggtgggc aatttcatt ttaaagagt taggc 2071
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 398
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
178 Met Asp Gly Val Thr Pro Thr Leu Ser Thr Ile Arg Gly Arg Thr Leu
179 1          5          10          15
182 Glu Ser Ser Thr Leu His Val Thr Pro Arg Ser Leu Asp Arg Asn Lys
183          20          25          30
186 Asp Gln Ile Thr Asn Ile Phe Ser Gly Phe Ala Gly Leu Leu Ala Ile
187          35          40          45
190 Leu Leu Val Val Ala Val Phe Cys Ile Leu Trp Asn Trp Asn Lys Arg
191          50          55          60
194 Lys Lys Arg Gln Val Pro Tyr Leu Arg Val Thr Val Met Pro Leu Leu
195 65          70          75          80
198 Thr Leu Pro Gln Thr Arg Gln Arg Ala Lys Asn Ile Tyr Asp Ile Leu
199          85          90          95
202 Pro Trp Arg Gln Glu Asp Leu Gly Arg His Glu Ser Arg Ser Met Arg
203          100          105          110
206 Ile Phe Ser Thr Glu Ser Leu Leu Ser Arg Asn Ser Glu Ser Pro Glu
207          115          120          125
210 His Val Pro Ser Gln Ala Gly Asn Ala Phe Gln Glu His Thr Ala His
211          130          135          140
214 Ile His Ala Thr Glu Tyr Ala Val Gly Ile Tyr Asp Asn Ala Met Val
215 145          150          155          160
218 Pro Gln Met Cys Gly Asn Leu Thr Pro Ser Ala His Cys Ile Asn Val
219          165          170          175

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222 Arg Ala Ser Arg Asp Cys Ala Ser Ile Ser Ser Glu Asp Ser His Asp
223           180           185           190
226 Tyr Val Asn Val Pro Thr Ala Glu Ile Ala Glu Thr Leu Ala Ser
227           195           200           205
230 Thr Lys Ser Pro Ser Arg Asn Leu Phe Val Leu Pro Ser Thr Gln Lys
231           210           215           220
234 Leu Glu Phe Thr Glu Glu Arg Asp Glu Gly Cys Gly Asp Ala Gly Asp
235 225           230           235           240
238 Cys Thr Ser Leu Tyr Ser Pro Gly Ala Glu Asp Ser Asp Ser Leu Ser
239           245           250           255
242 Asn Gly Glu Gly Ser Ser Gln Ile Ser Asn Asp Tyr Val Asn Met Thr
243           260           265           270
246 Gly Leu Asp Leu Ser Ala Ile Gln Glu Arg Gln Leu Trp Val Ala Phe
247           275           280           285
250 Gln Cys Cys Arg Asp Tyr Glu Asn Val Pro Ala Ala Asp Pro Ser Gly
251           290           295           300
254 Ser Gln Gln Gln Ala Glu Lys Asp Val Pro Ser Ser Asn Ile Gly His
255 305           310           315           320
258 Val Glu Asp Lys Thr Asp Asp Pro Gly Thr His Val Gln Cys Val Lys
259           325           330           335
262 Arg Thr Phe Leu Ala Ser Gly Asp Tyr Ala Asp Phe Gln Pro Phe Thr
263           340           345           350
266 Gln Ser Glu Asp Ser Gln Met Lys His Arg Glu Glu Met Ser Asn Glu
267           355           360           365
270 Asp Ser Ser Asp Tyr Glu Asn Val Leu Thr Ala Lys Leu Gly Gly Arg
271           370           375           380
274 Asp Ser Glu Gln Gly Pro Gly Thr Gln Leu Leu Pro Asp Glu
275 385           390           395

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278 <210> SEQ ID NO: 3

279 <211> LENGTH: 19

280 <212> TYPE: PRT

281 <213> ORGANISM: Homo sapiens

283 <400> SEQUENCE: 3

284 Gly Phe Ala Gly Leu Leu Ala Ile Leu Leu Val Val Ala Val Phe Cys

285 1 5 10 15

286 Ile Leu Trp

289 <210> SEQ ID NO: 4

290 <211> LENGTH: 40

291 <212> TYPE: PRT

292 <213> ORGANISM: Homo sapiens

294 <400> SEQUENCE: 4

295 Met Asp Gly Val Thr Pro Thr Leu Ser Thr Ile Arg Gly Arg Thr Leu

296 1 5 10 15

297 Glu Ser Ser Thr Leu His Val Thr Pro Arg Ser Leu Asp Arg Asn Lys

298 20 25 30

299 Asp Gln Ile Thr Asn Ile Phe Ser

300 35 40

303 <210> SEQ ID NO: 5

304 <211> LENGTH: 16

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305 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapiens
308 <400> SEQUENCE: 5
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310 1          5          10          15
313 <210> SEQ ID NO: 6
314 <211> LENGTH: 16
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <400> SEQUENCE: 6
319 Met Asp Gly Val Thr Pro Thr Leu Ser Thr Ile Arg Gly Arg Thr Cys
320 1          5          10          15
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324 <211> LENGTH: 24
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Description of artificial sequence: forward primer
331 <400> SEQUENCE: 7
332 ccatacctcct ggtcgttgcg gttt                24
336 <210> SEQ ID NO: 8
337 <211> LENGTH: 25
338 <212> TYPE: DNA
339 <213> ORGANISM: Artificial sequence
341 <220> FEATURE:
342 <223> OTHER INFORMATION: Description of artificial sequence: reverse primer
344 <400> SEQUENCE: 8
345 ttctgtcgc caaggcaaga tgtca                25

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VERIFICATION SUMMARY

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Input Set : N:\AMC\538370.txt

Output Set: N:\CRF4\06282005\J538370.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35